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DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE DNA polymerase theta.
GN POLO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Abbas A.R., Linn S.M.;
RT "Homo sapiens polymerase (DNA-directed), theta (POLO), mRNA.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY032677; AAK9635.1;
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001098; DNA_pol.
DR InterPro: IPR001650; Helicase_C.
DR Pfam: PF00270; DEAD.1.
DR Pfam: PF00476; DNA_pol_A.1.
DR Pfam: PF00271; helicase_C.1.
DR PROSITE: PS00447; DNA_POLYMERASE_A; UNKNOWN_1.
KM APP-binding: Helicase.
SQ SEQUENCE 2724 AA; 305148 MW; 30B8663614E65DC CRC64;

Query Match 18.1%; Score 75.5; DB 4; Length 2724;
Best Local Similarity 28.9%; Pred. No. 7.6;
Matches 24; Conservative 13; Mismatches 25; Indels 21; Gaps 3;

QY 20 LGDARLC-LRKTQOQKEQOILROSEVLFRTSEY-----LRKTGKGR 61
DB 86 LGERRKLCKIRKEHMEDEVRSQCAVILPRGRTLGIMLALIGREFAMILLRSRGR 145
QY 62 RMGSGQ---GGRGGTADTGMFLS 81
DB 146 SESGSDSFGSGGSDSSASPOFLS 168

RESULT 3
Q9NEB6 PRELIMINARY; PRT; 1254 AA.
AC Q9NEB6;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Kinesin-like protein.
GN L8325.12.
OS Leishmania major.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RA Straub-Friedlin;
RA Bothe G., Pohl T., Ivens A.C., Quall M., Rajandream M.A.,
RA Batteall B.G.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-FRIEDLIN;
RX MEDLINE-98146435; PubMed-9477341;
RA Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
RA Smith D.F.;
RT "A physical map of the Leishmania major Friedlin genome.";
RL Genome Res. 8:135-145(1998).
DR EMBL: AL157415; CAB75639.1;
DR HSP: P17119; 3KAR.
DR InterPro: IPR001752; kinesin_motor.
DR Pfam: PF00225; kinesin.1.
DR SMART: SM00129; KISC.1.
DR PROSITE: PS00411; KINESIN_MOTOR_DOMAIN1; 1.
DR PROSITE: PS50067; KINESIN_MOTOR_DOMAIN2; 1.
KM APP-binding: Coiled coil; Microtubules; Motor protein.
SQ SEQUENCE 1254 AA; 132206 MW; 79350B2F8C8B20A CRC64;

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Query Match 17.7%; Score 74; DB 5; Length 1254;
Best Local Similarity 33.9%; Pred. No. 4.9;
Matches 20; Conservative 10; Mismatches 27; Indels 2; Gaps 1;

QY 12 PIYFLSYLGDRLRLCKRTQOQKEQOILROSEVLFRTSEYLRRTGKGRMGCGG 70
DB 847 YTWVLECHLGYFAAMIRHOQOORORO--RLSGTLTTSASMRVYSSRSRSGG 903

RESULT 4
Q9ILC6 PRELIMINARY; PRT; 480 AA.
AC Q9ILC6;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE ORF119, gene family 8.
OS White spot syndrome virus (WSSV).
OC Viruses; unclassified viruses.
OX NCBI_TaxID=92652;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21342572; PubMed-11448154;
RA van Hulten M.C.W., Witteveldt J., Peters S., Kloosterboer N.,
RA Tarchini R., Fiers M., Sandbriek H., Lankhorst R.K., Vlak J.M.;
RT "The white spot syndrome virus DNA genome sequence.";
RL Virology 286:7-22(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA van Hulten M.C.W., Witteveldt J., Peters S., Kloosterboer N.,
RA Tarchini R., Fiers M., Sandbriek H., Lankhorst R.K., Vlak J.M.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF369029; AAK77788.1;
SQ SEQUENCE 480 AA; 51006 MW; 78091EAC58E861B CRC64;

Query Match 17.5%; Score 73; DB 12; Length 480;
Best Local Similarity 27.0%; Pred. No. 2.3;
Matches 20; Conservative 19; Mismatches 35; Indels 0; Gaps 0;

QY 3 LSTHFLFYLFYFLSYSLGRRRLCKRTQOQKEQOILROSEVLFRTSEYLRRTGKGR 62
DB 6 IATSLVFFFLFLVSTIILDGAKTIDSPRRKRRKRRYRTSGSDIGDTGTNGGG 65
QY 63 WGGGGRGRTADTG 76
DB 66 GGGGGGGGTNGNG 79

RESULT 5
Q8VAV1 PRELIMINARY; PRT; 486 AA.
AC Q8VAV1;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE WSV238 (WSSV294).
OS White spot syndrome virus (WSSV).
OC Viruses; unclassified viruses.
OX NCBI_TaxID=92652;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21548311; PubMed-11689662;
RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
RT "Complete genome sequence of the shrimp white spot bacilliform
RT virus.";
RL J. Virol. 75:11811-11820(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
SQ SEQUENCE FROM N.A.

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	Query Match	17.5%	Score 73:	DB 12;	Length 486;
	Best Local Similarity	27.0%;	Pred. No. 2,3;		
	Matches	20;	Conservative 19;	Mismatches 35;	Indels 0; Gaps 0;
QY	3 LSTHLFLYLFYFELSYSLGDRARCLNRKTKQOKEQLROSEVLYFRSETLRKGGKR	62			
	: : : : : : : : : : : : : : : : : : : : : :				
Dd	6 IATLVLFEEFLFFSITLLDGAKTIDSPFKRRRKKRYRTSGSDGIDGGTGTTNGGG	65			
	: : : : : : : : : : : : : : : : : : : : : :				
QY	63 WGGGGGRGTADTG	76			
	: : : : : : : : : : : : : : : : : : : : : :				
db	66 GGEGGGGGGTNGG	79			
	: : : : : : : : : : : : : : : : : : : : : :				

[illegible]

NCBI_TaxID=39947;
[1]
SEQUENCE FROM N.A.
STRAIN-CV. NIPPOBARE;
Buell C.R., Yuan O., Ouyang S., Liu J., Gansberger K., Kim M.M.,
Oveton II L.L., Bera J.J., Taitlin T., Krol M.I., Jarrah B.B.,
Jin S.S., Koo H., Zisman V., Hsieh S., Vanaken S.S.,
Utterback T.T., Feldlyum T.V., Yang O.Q., Haas B.J., Suh B.B.,
Peterson J.J., Quackenbush J., White O., Salzberg S.L., Frazer C.M.;
"Oryza sativa chromosome 10 BAC OSUNB004802Z genomic sequence."
Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
EMBL; AC099325; AAM18766.1; -
Polyprotein.
SO SEQUENCE 1150 AA; 126175 MW; 48533604BF3D620 CRC64;
Query Match 16.6%; Score 69.5; DB 10; Length 1150;
Best Local Similarity 29.3%; Pred. NO. 15;
Matches 22; Conservative 7; Mismatches 33; Indels 13; Gaps 1
QY 16 LVSLSGDRARCLRTKQKQEQILIROSEVL-----FRSETLKTKGRKR 62
DB 86 LSVLLSLARELLTQVSIETFAELRLLENMLCSQTENYHKMNSFSDMAVTTRKGRS 145
QY 63 WGGCGGRCGTADTG 77
DB 146 GGGRGRRGGNRRG 160
RESULT 10
ID Q94E54 PRELIMINARY; PRT; 203 AA.
AC Q94E54;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative THYS protein.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartidae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. NIPPOBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
clone.OSUNBa0089K24.";
RL Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.
RE EMBL; AP003215; BAB62558.1; -
DR InterPro: IPR004827; TR_bZIP.
DR Pfam; PF00170; bZIP. 1.
DR PROSITE; PS00036; BZIP_BASIC; UNKNOWN_1.
SO SEQUENCE 203 AA; 21092 MW; C796B3659CD9255F CRC64;
Query Match 16.5%; Score 69; DB 10; Length 203;
Best Local Similarity 26.4%; Pred. NO. 2.6;
Matches 24; Conservative 13; Mismatches 22; Indels 32; Gaps 3
QY 19 SLGDRARCLRK-----TKQQKEEQ-----TLROSEVLFSETLRK--- 55
DB 105 SAGCKEQRRLRLRNRYSAOARAKAYMTLEAKAKDELRNAELEORVSTLNENN 164
QY 56 -----TGKKGRMGOGSGRGSTADTG 77
DB 165 TLROIILNTTAHAGKRGSGGGGGGGG 195
RESULT 11
ID Q9SNUG PRELIMINARY; PRT; 296 AA.
AC Q9SNUG;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

QY 7 LFIYLFYFYL---SYSGDARALCLRTKQOQKEQOILROSEVLFSEITLRTGKGRW 63
DB 4 LHVILSLFLLPLPFSLSTSA-FCKRRWRQRR-----RRWRREGRRW 45
QY 64 ---GGOGGRC 70
DB 46 RHWGGGDDRG 56

RESULT 14

ID 050357 PRELIMINARY; PRT; 165 AA.
AC 050357;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CCPA & tnp genes (Fragment).
OS Lactobacillus casei.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Lactobacillaceae; Lactobacillus.
OX NCBI_TaxID=1582;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 393;
RX MEDLINE=98012962; PubMed=9352913;
RA Monedero V., Gosalbes M.U., Perez-Martinez G.;
RT "Cataloille repression in Lactobacillus casei ATCC393 is mediated by
CPA.";
RL J. Bacteriol. 179:6657-6664(1997).
DR EMBL; AJ003194; CAA05974.1; -.
FT NON TER 1
SQ SEQUENCE 165 AA; 16851 MW; C54BDC033EE93AC CRC64;

Query Match 16.3%; Score 68; DB 2; Length 165;
Best Local Similarity 35.7%; Pred. No. 2.8;
Matches 15; Conservative 6; Mismatches 21; Indels 0; Gaps 0;

QY 35 QKEQQLROSEVLFSEITLRTGKGRWGOGGRCGTADTG 76
DB 88 QQNGGTSENPARKVPPOTGTGGSGNDRTGTGTETG 129

RESULT 15

ID 08R1S6 PRELIMINARY; PRT; 429 AA.
AC 08R1S6;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 48.0 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024127; AAH24127.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 429 AA; 47964 MW; 40ABE564EB1BBEA CRC64;

Query Match 16.3%; Score 68; DB 11; Length 429;
Best Local Similarity 21.1%; Pred. No. 7.9;
Matches 20; Conservative 24; Mismatches 29; Indels 22; Gaps 2;

QY 3 LSTHLFIYLFYFLSLSDRARL-----CLRTKQOQKEQOILR 42
DB 20 ISEHCDLIFAFDEIYALGYRENVNLAQIRTFEMDSHEKVFRAVETQERAKEMRR 79
QY 43 QSEVLFSEITLRTGKGRWGOGGRCGTADTG 77

DB 80 KANEL--QOARRDAEROGKAPGFGGSSAVSGG 112

Search completed: May 29, 2003, 15:20:14
Job time : 88 secs